

# Sequence Alignment #2

## RESULT 4

AQ480395/c

LOCUS AQ480395 522 bp DNA linear GSS 23-APR-1999

DEFINITION RPCI-11-236B22.TV RPCI-11 Homo sapiens genomic clone

RPCI-11-236B22, genomic survey sequence.

ACCESSION AQ480395

VERSION AQ480395.1 GI:4662514

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 522)

AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and  
Venter, J.C.

TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready  
Map Building

JOURNAL Unpublished (1997)

COMMENT Other\_GSSs: RPCI-11-236B22.TJ

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Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from

Research Genet cs ([info@resgen.com](mailto:info@resgen.com)). BAC end search page:

[http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html).

Seq primer: T7

Class: BAC ends.

FEATURES Location/Qualifiers

source

1..522

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="GDB:7590285"

/db\_xref="taxon:9606"

/clone="RPCI-11-236B22"

/sex="Male"

/cell\_type="Lymphocytes"

/clone\_lib="RPCI-11"

/note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;

RPCI11 Human Male BAC Library"

## ORIGIN

Query Match 28.5%; Score 231; DB 15; Length 522;

Best Local Similarity 98.8%; Pred. No. 2.3e-55;

Matches 244; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 ACAGGTGTAAGCCACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCA 60

|||||

Db 247 ACAGGTGTAAGCCACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCA 188

Qy	61	CTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAG	120
Db	187	CTCTGATCCATTTTGAAGTAAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAG	128
Qy	121	CATGTCATGTGCTA---ATGGCCAGTGACATCATAAAAGAAAAGTGCATTACTGAATGCT	177
Db	127	CATGTCATGTGCTAATTATGGCCAGTGACATCATAAAAGAAAAGTGCATTACTGAATGCT	68
Qy	178	TTCAATTTCTTATAATGATGGTAAGGTGGCATGTCATGGGGCCTATTTAGCCCCAGACAT	237
Db	67	TTCAATTTCTTATAATGATGGTAAGGTGGCATGTCATGGGGCCTATTTAGCCCCAGACAT	8
Qy	238	CACTCCA	244
Db	7	CACTCCA	1